

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model1

Run on: April 19, 2005, 10:47:57 ; Search time 136 Seconds

(without alignments)
928.683 Million cell updates/sec

Title: US-09-714-792a-4

Perfect score: 2104

Sequence: 1 MAFVCLAIIGLYTFLISTTF.....LLAKRPTVPMIEFFCDT 380

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/prodata/2/pubppa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/2/pubppa/PCT_NEW_PUB.pep:*
3: /cgn2_6/prodata/2/pubppa/US06_NEW_PUB.pep:*
4: /cgn2_6/prodata/2/pubppa/US06_PUBCOMB.pep:*
5: /cgn2_6/prodata/2/pubppa/US07_NEW_PUB.pep:*
6: /cgn2_6/prodata/2/pubppa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/prodata/2/pubppa/US08_NEW_PUB.pep:*
8: /cgn2_6/prodata/2/pubppa/US08_PUBCOMB.pep:*
9: /cgn2_6/prodata/2/pubppa/US09_PUBCOMB.pep:*
10: /cgn2_6/prodata/2/pubppa/US09B_PUBCOMB.pep:*
11: /cgn2_6/prodata/2/pubppa/US09C_PUBCOMB.pep:*
12: /cgn2_6/prodata/2/pubppa/US09_NEW_PUB.pep:*
13: /cgn2_6/prodata/2/pubppa/US10_PUBCOMB.pep:*
14: /cgn2_6/prodata/2/pubppa/US10B_PUBCOMB.pep:*
15: /cgn2_6/prodata/2/pubppa/US10C_PUBCOMB.pep:*
16: /cgn2_6/prodata/2/pubppa/US10D_PUBCOMB.pep:*
17: /cgn2_6/prodata/2/pubppa/US10E_PUBCOMB.pep:*
18: /cgn2_6/prodata/2/pubppa/US11_NEW_PUB.pep:*
19: /cgn2_6/prodata/2/pubppa/US60_NEW_PUB.pep:*
20: /cgn2_6/prodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2104	100.0	380	8 US-08-815-773-2	Sequence 2, Appl1
2	2104	100.0	380	9 US-08-871-617-2	Sequence 2, Appl1
3	2104	100.0	380	9 US-09-780-926-1	Sequence 1, Appl1
4	2104	100.0	380	10 US-09-090-867-2	Sequence 1, Appl1
5	2104	100.0	380	13 US-10-104-408-1	Sequence 2, Appl1
6	2104	100.0	380	16 US-10-887-865-2	Sequence 1, Appl1
7	2104	100.0	380	17 US-10-887-863-2	Sequence 2, Appl1
8	2104	100.0	380	17 US-10-941-486-1	Sequence 1, Appl1
9	2078	98.8	380	8 US-08-815-773-4	Sequence 4, Appl1
10	2078	98.8	380	10 US-09-090-867-4	Sequence 4, Appl1
11	2078	98.8	380	16 US-10-887-865-4	Sequence 4, Appl1
12	2078	98.8	380	17 US-10-887-863-4	Sequence 4, Appl1
13	1853	88.1	372	8 US-08-815-773-7	Sequence 7, Appl1

14	1853	88.1	372	10 US-09-090-867-7	Sequence 7, Appl1
15	1853	88.1	372	16 US-10-887-865-7	Sequence 7, Appl1
16	1853	88.1	372	17 US-10-887-863-7	Sequence 7, Appl1
17	1764	83.8	317	9 US-09-825-561A-84	Sequence 84, Appl1
18	1503	71.4	386	9 US-09-828-995B-61	Sequence 61, Appl1
19	1503	71.4	386	16 US-10-753-159-61	Sequence 61, Appl1
20	1452.5	69.0	365	9 US-09-828-995B-66	Sequence 66, Appl1
21	1452.5	69.0	365	16 US-10-753-159-66	Sequence 66, Appl1
22	1392.5	66.2	318	9 US-09-828-995B-69	Sequence 69, Appl1
23	1392.5	66.2	318	16 US-10-753-159-69	Sequence 69, Appl1
24	1392.5	66.2	561	9 US-09-828-995B-72	Sequence 72, Appl1
25	1392.5	66.2	561	16 US-09-828-995B-81	Sequence 81, Appl1
26	1392.5	66.2	561	16 US-10-753-159-81	Sequence 81, Appl1
27	1392.5	66.2	561	16 US-10-753-159-81	Sequence 81, Appl1
28	1392.5	66.2	563	9 US-09-828-995B-78	Sequence 78, Appl1
29	1392.5	66.2	563	16 US-10-753-159-78	Sequence 78, Appl1
30	1392.5	66.2	565	9 US-09-828-995B-75	Sequence 75, Appl1
31	1392.5	66.2	565	16 US-10-753-159-75	Sequence 75, Appl1
32	935.5	44.5	255	9 US-09-828-995B-58	Sequence 58, Appl1
33	935.5	44.5	255	16 US-10-753-159-58	Sequence 58, Appl1
34	626.5	29.8	145	9 US-09-828-995B-55	Sequence 55, Appl1
35	626.5	29.8	145	16 US-10-753-159-55	Sequence 55, Appl1
36	310.5	14.8	420	9 US-09-886-319A-24	Sequence 24, Appl1
37	310.5	14.8	420	14 US-10-376-564-24	Sequence 24, Appl1
38	302.5	14.4	405	9 US-09-828-995B-50	Sequence 50, Appl1
39	302.5	14.4	405	16 US-10-753-159-50	Sequence 50, Appl1
40	296	14.1	426	13 US-10-036-568-2	Sequence 2, Appl1
41	295.5	14.0	427	15 US-10-671-697-9	Sequence 9, Appl1
42	293	13.9	313	14 US-10-283-349-106	Sequence 106, Appl1
43	290.5	13.8	426	13 US-10-036-568-4	Sequence 4, Appl1
44	288.5	13.7	427	17 US-10-850-270-4	Sequence 4, Appl1
45	288	13.7	780	9 US-09-935-868-38	Sequence 38, Appl1

ALIGNMENTS

RESULT 1
US-08-815-773-2
Sequence 2, Application US/08815773
Publication No. US20030100046A1
GENERAL INFORMATION:
APPLICANT: Baumgartner, James W.
APPLICANT: Parrish, Theresa M.
APPLICANT: Foster, Donald C.
APPLICANT: Grant, Frank J.
APPLICANT: O'Hara, Patrick J.
TITLE OF INVENTION: Testis-Specific Receptor
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815, 773
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E.
REGISTRATION NUMBER: 31,648
REFERENCE/DOCKET NUMBER: 95-33
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-815-773-2

Query Match 100.0%; Score 2104; DB 8; Length 380;
Best Local Similarity 100.0%; Pred. No. 3e-176;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIIGCLYTLISTFTGCTSSDTEIKVNPDPDFEIVDPGLYLYQWQPPSLD 60
DB 1 MAFVCLAIIGCLYTLISTFTGCTSSDTEIKVNPDPDFEIVDPGLYLYQWQPPSLD 60
QY 61 HFKECTVEYELKYNIGSEMTKTIITKNLHYKDGFDLNGKIEAKIHTLLPWOCTNGSEVQ 120
DB 61 HFKECTVEYELKYNIGSEMTKTIITKNLHYKDGFDLNGKIEAKIHTLLPWOCTNGSEVQ 120
QY 121 SSMATTYWIISPGIPEFTKVQDMDCVYNNWOYLLCSMKPGIGVLLDTNVLNLFYWEGLDH 180
DB 121 SSMATTYWIISPGIPEFTKVQDMDCVYNNWOYLLCSMKPGIGVLLDTNVLNLFYWEGLDH 180
QY 181 ALQCVDIYKADGQNIIGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLONIIVKPLP 240
DB 181 ALQCVDIYKADGQNIIGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLONIIVKPLP 240
QY 241 PVYLFTRESSCEIKLWMSIPLGPIPARCFDYEIEIREDDTLVTAVENTETTLKTNE 300
DB 241 PVYLFTRESSCEIKLWMSIPLGPIPARCFDYEIEIREDDTLVTAVENTETTLKTNE 300
QY 301 TROLCFVRSKVNIIYCSDDGIWSEMSDYQCEGEBLSKTLRLPWLPGFILLIIVIPVTG 360
DB 301 TROLCFVRSKVNIIYCSDDGIWSEMSDYQCEGEBLSKTLRLPWLPGFILLIIVIPVTG 360
QY 361 LLRKRPNTYPMIPEFFCDT 380
DB 361 LLRKRPNTYPMIPEFFCDT 380

RESULT 2

US-09-871-617-2
Sequence 2, Application US/09871617
Patent No. US20020072090A1

GENERAL INFORMATION:

APPLICANT: Jing-Shan Hu and Edward Appelbaum
TITLE OF INVENTION: HR-1 RECEPTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA

ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/871,617
FILING DATE: 04-Jun-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/871,122
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,344

REFERENCE/DOCKET NUMBER: ATG50007P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219

TELEFAX: 610-270-5090
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
TYPE: amino acid
STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-871-617-2
Query Match 100.0%; Score 2104; DB 9; Length 380;
Best Local Similarity 100.0%; Pred. No. 3e-176;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIIGCLYTLISTFTGCTSSDTEIKVNPDPDFEIVDPGLYLYQWQPPSLD 60
DB 1 MAFVCLAIIGCLYTLISTFTGCTSSDTEIKVNPDPDFEIVDPGLYLYQWQPPSLD 60
QY 61 HFKECTVEYELKYNIGSEMTKTIITKNLHYKDGFDLNGKIEAKIHTLLPWOCTNGSEVQ 120
DB 61 HFKECTVEYELKYNIGSEMTKTIITKNLHYKDGFDLNGKIEAKIHTLLPWOCTNGSEVQ 120
QY 121 SSMATTYWIISPGIPEFTKVQDMDCVYNNWOYLLCSMKPGIGVLLDTNVLNLFYWEGLDH 180
DB 121 SSMATTYWIISPGIPEFTKVQDMDCVYNNWOYLLCSMKPGIGVLLDTNVLNLFYWEGLDH 180
QY 181 ALQCVDIYKADGQNIIGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLONIIVKPLP 240
DB 181 ALQCVDIYKADGQNIIGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLONIIVKPLP 240
QY 241 PVYLFTRESSCEIKLWMSIPLGPIPARCFDYEIEIREDDTLVTAVENTETTLKTNE 300
DB 241 PVYLFTRESSCEIKLWMSIPLGPIPARCFDYEIEIREDDTLVTAVENTETTLKTNE 300
QY 301 TROLCFVRSKVNIIYCSDDGIWSEMSDYQCEGEBLSKTLRLPWLPGFILLIIVIPVTG 360
DB 301 TROLCFVRSKVNIIYCSDDGIWSEMSDYQCEGEBLSKTLRLPWLPGFILLIIVIPVTG 360
QY 361 LLRKRPNTYPMIPEFFCDT 380
DB 361 LLRKRPNTYPMIPEFFCDT 380

RESULT 3

US-09-780-926-1
Sequence 1, Application US/09780926
Publication No. US20020197266A1

GENERAL INFORMATION:

APPLICANT: The Penn State Research Foundation
TITLE OF INVENTION: IMMUNOTHERAPY USING INTERLEUKIN 13 RECEPTOR SUBUNIT ALPHA
FILE REFERENCE: 6460-32
CURRENT APPLICATION NUMBER: US/09/780,926
CURRENT FILING DATE: 2000-02-08
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.0

SEQ ID NO 1
LENGTH: 380
TYPE: PRT
ORGANISM: Homo sapiens
US-09-780-926-1

Query Match 100.0%; Score 2104; DB 9; Length 380;
Best Local Similarity 100.0%; Pred. No. 3e-176;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIIGCLYTLISTFTGCTSSDTEIKVNPDPDFEIVDPGLYLYQWQPPSLD 60

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 19, 2005, 10:39:21 ; Search time 43 Seconds

(Without alignments)
659,689 Million cell updates/sec

Title: US-09-714-792A-4

Perfect score: 2104
Sequence: 1 MARVCAIGGLYFLSTTF.....LLRKPTYPKMIPEFCDT 380

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodaca/1/1aa/5A COMB pep:*
- 2: /cgn2_6/prodaca/1/1aa/5B COMB pep:*
- 3: /cgn2_6/prodaca/1/1aa/6A COMB pep:*
- 4: /cgn2_6/prodaca/1/1aa/6B COMB pep:*
- 5: /cgn2_6/prodaca/1/1aa/PCUS COMB pep:*
- 6: /cgn2_6/prodaca/1/1aa/backfile1.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2104	100.0	380	1 US-08-609-572-4	Sequence 4, Appl
2	2104	100.0	380	3 US-08-841-751-4	Sequence 4, Appl
3	2104	100.0	380	3 US-08-846-340-4	Sequence 4, Appl
4	2104	100.0	380	3 US-08-846-344-4	Sequence 4, Appl
5	2104	100.0	380	3 US-09-301-808-4	Sequence 4, Appl
6	1764	83.8	317	4 US-09-825-561A-84	Sequence 6, Appl
7	1503	71.4	386	4 US-09-828-995B-61	Sequence 6, Appl
8	1452.5	69.0	386	4 US-09-828-995B-66	Sequence 6, Appl
9	1392.5	66.2	318	4 US-09-828-995B-69	Sequence 6, Appl
10	1392.5	66.2	351	4 US-09-828-995B-72	Sequence 6, Appl
11	1392.5	66.2	551	4 US-09-828-995B-81	Sequence 8, Appl
12	1392.5	66.2	553	4 US-09-828-995B-78	Sequence 8, Appl
13	1392.5	66.2	555	4 US-09-828-995B-75	Sequence 8, Appl
14	1194.5	56.8	383	1 US-08-609-572-2	Sequence 2, Appl
15	1194.5	56.8	383	3 US-08-841-751-2	Sequence 2, Appl
16	1194.5	56.8	383	3 US-08-846-340-2	Sequence 2, Appl
17	1194.5	56.8	383	3 US-08-846-344-2	Sequence 2, Appl
18	1194.5	56.8	383	3 US-09-301-808-2	Sequence 2, Appl
19	955	45.4	220	4 US-09-949-016-7266	Sequence 7266, Ap
20	935.5	44.5	255	4 US-09-828-995B-58	Sequence 58, Ap
21	626.5	29.8	145	4 US-09-828-995B-55	Sequence 55, Appl
22	311.5	14.8	420	1 US-07-757-390-13	Sequence 13, Appl
23	311.5	14.8	420	1 US-08-442-282-13	Sequence 13, Appl
24	311.5	14.8	420	1 US-08-442-281-13	Sequence 13, Appl
25	310.5	14.8	420	2 US-08-939-727-13	Sequence 14, Appl
26	310.5	14.8	396	1 US-07-757-390-14	Sequence 14, Appl
27	310.5	14.8	396	1 US-08-442-282-14	Sequence 14, Appl

28	310.5	14.8	396	1 US-08-442-281-14	Sequence 14, Appl
29	310.5	14.8	396	2 US-08-939-727-14	Sequence 14, Appl
30	310.5	14.8	420	4 US-09-886-319A-24	Sequence 24, Appl
31	310.5	14.8	420	4 US-09-949-016-5958	Sequence 5958, Ap
32	310.5	14.8	427	4 US-09-949-016-8614	Sequence 8614, Ap
33	310.5	14.8	427	4 US-09-949-016-8620	Sequence 8620, Ap
34	302.5	14.4	405	4 US-09-828-995B-50	Sequence 50, Appl
35	295.5	14.0	427	3 US-08-969-125-9	Sequence 9, Appl
36	295.5	14.0	427	4 US-09-545-002-9	Sequence 9, Appl
37	295.5	14.0	427	4 US-09-949-016-6094	Sequence 6094, Ap
38	293	13.9	313	3 US-08-836-561-106	Sequence 106, App
39	293	13.9	313	4 US-09-434-122-106	Sequence 106, App
40	292	13.9	335	1 US-07-947-130-2	Sequence 2, Appl
41	292	13.9	335	1 US-08-421-822-2	Sequence 2, Appl
42	292	13.9	335	1 US-08-421-823-2	Sequence 2, Appl
43	285	13.5	793	4 US-09-313-942-32	Sequence 32, Appl
44	284	13.5	322	4 US-09-825-561A-82	Sequence 82, Appl
45	284	13.5	784	4 US-09-313-942-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-08-609-572-4
Sequence 4, Application US/08609572
Patent No. 5710023
GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Donaldson, Debra
APPLICANT: Pitz, Lori
APPLICANT: Neven, Tamlyn
APPLICANT: Whitlers, Matthew
APPLICANT: Wood, Clive
TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM: Floppy disk
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,572
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-609-572-4
Query Match 100.0%; Score 2104; DB 1; Length 380;
Best Local Similarity 100.0%; Pred. No. 2.2e-207; Indels 0; Gaps 0;
Matches 380; Conservative 0; Mismatches 0;
1 MARVCAIGGLYFLSTTFGCTSSDTEIKVNPDPDEFIVDVGXYGLYIQNPPLSLD 60
|||||

Db 1 MAPVCLAIIGCLYTLFTSTGCTSSSDTEIKVNPDPDFEIVDPGLYGLYLQMPPLSLD 60
QY 61 HFKECTVEYELKYNIGSETWKTIIITKNLHYKQDFLNGKIEAKIHTLLPMQCTNGSEVQ 120
Db 61 HFKECTVEYELKYNIGSETWKTIIITKNLHYKQDFLNGKIEAKIHTLLPMQCTNGSEVQ 120
QY 121 SSMAETTYWISPGQIPETKVDMDCCVYNNQYLLCSMKRPGIGVLLDTNNLFFYBEGLDH 180
Db 121 SSMAETTYWISPGQIPETKVDMDCCVYNNQYLLCSMKRPGIGVLLDTNNLFFYBEGLDH 180
QY 181 ALOCVDYIKADGQNIIGCRFPYLBASDYKDFYICVNGSSENKPIRSSYFTFOLQNIIVPLP 240
Db 181 ALOCVDYIKADGQNIIGCRFPYLBASDYKDFYICVNGSSENKPIRSSYFTFOLQNIIVPLP 240
QY 241 PVYLTFTRESSCEIKLWMSIPLGPIPARCFDYIEIREDDTTLVATVENEETTLTKTNE 300
Db 241 PVYLTFTRESSCEIKLWMSIPLGPIPARCFDYIEIREDDTTLVATVENEETTLTKTNE 300
QY 301 TROLCFVVRSKVNIYCSDDGIWSEMSDKQCEGEBLSKTLRLPWLPGFLLIVIFVTG 360
Db 301 TROLCFVVRSKVNIYCSDDGIWSEMSDKQCEGEBLSKTLRLPWLPGFLLIVIFVTG 360
QY 361 LLARKPNTYPMIPEPFCDT 380
Db 361 LLARKPNTYPMIPEPFCDT 380

RESULT 2

US-08-841-751-4
Sequence 4, Application US/08841751
Patent No. 6214559

GENERAL INFORMATION:

APPLICANT: Collins, Mary

APPLICANT: Donaldson, Debra

APPLICANT: Fitz, Lori

APPLICANT: Neben, Tamlyn

APPLICANT: Whiters, Matthew

APPLICANT: Wood, Clive

TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESS: Genetics Institute, Inc.

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: MA

COUNTRY: USA

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/841,751

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/609,572

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

REFERENCE/DOCKET NUMBER: G15268

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO. 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 380 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

Query Match 100.0%; Score 2104; DB 3; Length 380;
Best Local Similarity 100.0%; Pred. No. 2.2e-207; Mismatches 0; Gaps 0;
Matches 380; Conservative 0; Indels 0; Gaps 0;
QY 1 MAPVCLAIIGCLYTLFTSTGCTSSSDTEIKVNPDPDFEIVDPGLYGLYLQMPPLSLD 60
Db 1 MAPVCLAIIGCLYTLFTSTGCTSSSDTEIKVNPDPDFEIVDPGLYGLYLQMPPLSLD 60
QY 61 HFKECTVEYELKYNIGSETWKTIIITKNLHYKQDFLNGKIEAKIHTLLPMQCTNGSEVQ 120
Db 61 HFKECTVEYELKYNIGSETWKTIIITKNLHYKQDFLNGKIEAKIHTLLPMQCTNGSEVQ 120
QY 121 SSMAETTYWISPGQIPETKVDMDCCVYNNQYLLCSMKRPGIGVLLDTNNLFFYBEGLDH 180
Db 121 SSMAETTYWISPGQIPETKVDMDCCVYNNQYLLCSMKRPGIGVLLDTNNLFFYBEGLDH 180
QY 181 ALOCVDYIKADGQNIIGCRFPYLBASDYKDFYICVNGSSENKPIRSSYFTFOLQNIIVPLP 240
Db 181 ALOCVDYIKADGQNIIGCRFPYLBASDYKDFYICVNGSSENKPIRSSYFTFOLQNIIVPLP 240
QY 241 PVYLTFTRESSCEIKLWMSIPLGPIPARCFDYIEIREDDTTLVATVENEETTLTKTNE 300
Db 241 PVYLTFTRESSCEIKLWMSIPLGPIPARCFDYIEIREDDTTLVATVENEETTLTKTNE 300
QY 301 TROLCFVVRSKVNIYCSDDGIWSEMSDKQCEGEBLSKTLRLPWLPGFLLIVIFVTG 360
Db 301 TROLCFVVRSKVNIYCSDDGIWSEMSDKQCEGEBLSKTLRLPWLPGFLLIVIFVTG 360
QY 361 LLARKPNTYPMIPEPFCDT 380
Db 361 LLARKPNTYPMIPEPFCDT 380

RESULT 3

US-08-846-340-4
Sequence 4, Application US/08846340
Patent No. 6248714

GENERAL INFORMATION:

APPLICANT: Collins, Mary

APPLICANT: Donaldson, Debra

APPLICANT: Fitz, Lori

APPLICANT: Neben, Tamlyn

APPLICANT: Whiters, Matthew

APPLICANT: Wood, Clive

TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESS: Genetics Institute, Inc.

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: MA

COUNTRY: USA

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/846,340

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/609,572

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

REFERENCE/DOCKET NUMBER: G15268

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851